

1 GCACGAGGAACAGAACACTTTTCTCATGTCCAGGGTCAGATTACAAGAGCACTCAAGACTT 60
61 TACTGACGAAAACCTCAGGAAATCCTCTATCACAAAGAGGTTTGGCAACTAACTAAGACA 120
121 TTAAAAGGAAAATACCAGATGCCACTCTGCAGGCTGCAATAACTACTACTTACTGGATAC 180
181 ATTCAAACCCTCCAGAATCAACAGTTATCAGGTAACCAACAAGAAATGCAAGCCGTCGAC 240
1 M Q A V D 5
241 AATCTCACCTCTGCGCCTGGGAACACCAGTCTGTGCACCAGAGACTACAAAATCACCCAG 300
6 N L T S A P G N T S L C T R D Y K I T Q 25
301 GTCCTCTTCCCACTGCTCTACACTGTCTGTTTTTTGTTGGACTTATCACAAATGGCCTG 360
26 V L F P L L Y T V L F F V G L I T N G L 45
361 GCGATGAGGATTTTCTTTCAAATCCGGAGTAAATCAAACCTTTATTATTTTCTTAAGAAC 420
46 A M R I F F Q I R S K S N F I I F L K N 65
421 ACAGTCATTTCTGATCTTCTCATGATTCTGACTTTTCCATTCAAATCTTAGTGATGCC 480
66 T V I S D L L M I L T F P F K I L S D A 85
481 AACTGGGAACAGGACCACTGAGAACTTTTGTGTGTCAAGTTACCTCCGTCATATTTTAT 540
86 K L G T G P L R T F V C Q V T S V I F Y 105
541 TTCACAATGTATATCAGTATTTTATTCTGGGACTGATAACTATCGATCGCTACCAGAAG 600
106 F T M Y I S I S F L G L I T I D R Y Q K 125
601 AcCACCAGGCCATTTAAAACATCCAACCCCAAAAATCTCTTGGGGGCTAAGATTCTCTCT 660
126 T T R P F K T S N P K N L L G A K I L S 145
661 GTTGTCTCTGGGCATTCATGTTCTTACTCTCTTtGCCTAACATGATTCTGACCAACAGg 720
146 V V I W A F M F L L S L P N M I L T N R 165
721 CAGCCGAGAGACAAGAATGTGaAGAAaTGCTCTTTCCTTAAATCAGAGTTCGGTCTAGTC 780
166 Q P R D K N V K K C S F L K S E F G L V 185
781 TGGCATGAAATAGTAAATTACATCTGTCAAGTCATTTTCTGGATTAATTTCTTAATTGTT 840
186 W H E I V N Y I C Q V I F W I N F L I V 205

FIG.1A

841	ATTGTATGTTATACACTCATTACAAAAGAACTGTACCGGTCATACGTAAGAACGAGGGGT	900
206	I V C Y T L I T K E L Y R S Y V R T R G	225
901	GTAGGTAAAGTCCCCAGGAAAAAGGTGAACGTCAAAGTTTTTCATTATCATTGCTGTATTC	960
226	V G K V P R K K V N V K V F I I I A V F	245
961	TTTATTTGTTTTGTTCTTTCCATTTTGCCCGAATTCCTTACACCCTGAGCCAAACCCGG	1020
246	F I C F V P F H F A R I P Y T L S Q T R	265
1021	GATGTCTTTGACTGCACtGcTGAAAATACTCTGTTCTATGTGAAAGAGAGCACTCTGTGG	1080
266	D V F D C T A E N T L F Y V K E S T L W	285
1081	TTAACTTCCTTAAATGCATGCCTGGATCCGTTCACTATTTTTTCTTTGCAAGTCCTTC	1140
286	L T S L N A C L D P F I Y F F L C K S F	305
1141	AGAAATTCCTTGATAAGTATGCTGAAGTGCCCCAATTCTGCAACATCTCTGTCCCAGGAC	1200
306	R N S L I S M L K C P N S A T S L S Q D	325
1201	AATAGGAAAAAAGAACAGGATGGTGGTGAcCCAAATGAAGAGACTCCAATGTAAACAAAT	1260
326	N R K K E Q D G G D P N E E T P M *	343
1261	TAAC TAAGGAAATATTTCAATCTCTTTGTGTT CAGAACTCGTTAAAGCAAAGCGCTAAGT	1320
1321	AAAAATATTA ACTGACGAAGAAGCAACTAAGTTAATAATAATGACTCTAAAGAAACAGAA	1380
1381	GATTACAAAAGCAATTTTCATTTACCTTTCCAGTATGAAAAGCTATCTTAAAATATAGAA	1440
1441	AACTAATCTAAACTGTAGCTGTATTAGCAGCAAAACAAACGACATCCAATTGTCATGCTG	1500
1501	CATGCAAAACTACACAGAATTCATGTTTTGgCAGAGTTTTGGCAAAATGAGTAATCATAT	1560
1561	AATATTTACTGTAATTTTTTAAAATACATTATCGTTCACAATTTTATTTTTTCATAATCAA	1620
1621	CTAAGGAAGAACGATCAATTGGATATAATCTTCTTACCAAAAATGATAGTTAAAATGTAT	1680
1681	ATATATCCTAGTCCCCTAACC aATCCTGACCTATTGGGATACTTATAAAAATTTAAGTA	1740
1741	AGTGGGATACACAAAGAATAATAACTATTA ACTTTTCATTATTAGCcAAAAACCTAAGGG	1800

FIG.1B

1801 ATTTAACTAATTGAAaCTGTATTTGATTGGACTTAATTTTTTATGTTTATTTAGAAGAT 1860
1861 AAAGATTTAAGAAGACCTTTACAATAAAGAGAAGAAATATCGAAGTCATTAAAATAAGGA 1920
1921 GACTTACTTTTATGACATTCTAATACTAAAAAATATAGAAATATTTCCCTTAATTCTAGAG 1980
1981 AACTAGTTTTACTAATTTTTTACAACCTCAATAATACCATCACTGACACTTACCTTTAT 2040
2041 TAATTAGCTTCTAGAAAATAGCTGCTAATTAGGTTAATGAACATTTTACCTTAGTGAAAA 2100
2101 AAAaTTAATTAAATATGATTACAAAGTTGCACAGCATAACTACTGAGAGGAAAGTGATTG 2160
2161 ATCTGTTTGTAATTACTTGTTTGTATTGGTGTGTATAAAATACAAATTTACATTAAACTC 2220
2221 TAAAtcattaaaAAAAAAAAAAAAAAAAA 2247

FIG.1C

781 CAAGGCCCGCCGCCTGCTGAAGACGGTGTGATGATCCTGCTGGCCTTCTTGGTGTGCTG 840
 245 K A R R L L K T V L M I L L A F L V C W 264

841 GGGACCACTCTTCGGGCTGCTGCTGGCCGACGTCTTTGGCTCCAACCTCTGGGCCCAGGA 900
 265 G P L F G L L L A D V F G S N L W A Q E 284

901 GTACCTGCGGGGCATGGACTGGATCCTGGCCCTGGCCGTCTCAACTCGGCGGTCAACCC 960
 285 Y L R G M D W I L A L A V L N S A V N P 304

961 CATCATCTACTCCTTCCGCAGCAGGGAGGTGTGCAGAGCCGTGCTCAGCTTCCTCTGCTG 1020
 305 I I Y S F R S R E V C R A V L S F L C C 324

1021 CGGGTGTCTCCGGCTGGGCATGCGAGGGCCCGGGGACTGCCTGGCCCGGGCCGTGAGGC 1080
 325 G C L R L G M R G P G D C L A R A V E A 344

1081 TCACTCCGGAGCTTCCACCACCGACAGCTCTCTGAGGCCAAGGGACAGCTTTCGCGGCTC 1140
 345 H S G A S T T D S S L R P R D S F R G S 364

1141 CCGCTCGCTCAGCTTTCGGATGCGGGAGCCCCTGTCCAGCATCTCCAGCGTGCGGAGCAT 1200
 365 R S L S F R M R E P L S S I S S V R S I 384

1201 CTGAAGTTGCAGTCTTGCGTGTGGATGGTGAACCACCGGGTGCGTGCCAGGCAGGCCCT 1260
 385 * 385

1261 CCTGGGGTACAGGAAGCTGTGTGCACGCAACCTCGCCCTGTATGGGGAGCAGGGAACGGG 1320

1321 ACAGGCCCCCATGGACTTGCCCGGTGGCCTCTCGGGGCTTCTGACGCCATATGGACTTGC 1380

1381 CCATTGCCTATGGCTCACCTGGACAAGGAGGCAACCACCCACCTCCCCGTAGGAGCAG 1440

1441 AGAGCACCTGGTGTGGGGGCGAGTGGGTTCCCCACAACCCCGCTTCTGTGTGATTCTGG 1500

1501 GGAAGTCCCGGCCCCCTCTCTGGGCCTCAGTAGGGCTCCAGGCTGCAAGGGGTGGACTGT 1560

1561 GGGATGCATGCCCTGGCAACATTGAAGTTCGATCATGGTAAAAAAAAAAAAAAAAAAAAA 1620

1621 AAAAAAAAAAAAAAAAAA 1637

FIG.3B

1	MNATGTPVAPES	CQQLAAGGHSRLIVLHYNHSGRLAGRGGPEDGGLGALR	50
1	MGPTSVPLVKAHRSSVSDYVNYDIIVRHYN	TGKLNISADKEN.SIKLTS	49
51	GLSVAASCLVVLENLLVLAAITSHMRSQRWVYYCLVNITMSDLLTGAAYL		100
50	VVFILICCFIILENIFVLLTIWKT	KKFHRPMYYFIGNLALSDDL	99
101	ANVLLSGARTFRLAPAQWFLRKGLLFTALAASTFSL	LFTAGLRFATMVRP	150
100	ANLLLSGATTYKLTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLKM		149
151	VAESGATKTSRVYGFIGLCWLLAALLGMLPLLGNCLCAFDR	CSSLLPLY	200
150	KLHNGS.NNFRLFL	LISACWVISLILGGLPIMGWNCISALSSCSTVLPLY	198
201	SKRYILFCLVIFAGVLATIMGLYGAI	FRLVQASGQKAPRPAARRKARR..	248
199	HKHYILFCTTVFTLLLLSIVILYCRIYSLVR	TRSRLTFRKNISKASRSS	248
249LLKTVLMILLAFLVCWGPLFGLLLADVFGSNLWAQEYLRGMDWILA		294
249	ENVALLKTVIIVLSVFIACWAPLFILLLLDV.GCKVK	TCDILFRAEYFLV	297
295	LAVLNSAVNP	IIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAVEA	344
298	LAVLNSGTNP	IIYTLTNKEMRRAFIRIMSCCKCPSG..DSAGKFKRPIIA	345
345	...HSGASTTDSSLRPRDSFRGSRSL	SFRMREPLSSIS	379
346	GMEFSRSKSDNSSHPQKDE..G	DNPETIMSSGNVNSSS	381

FIG.4